SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rnpn.

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-06
72.rnpn.

```
                          GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          June  6, 2006, 17:16:35 ; Search time 146 Seconds
                                           (without alignments)
                                           2307.745 Million cell updates/sec

Title:           US-10-063-581-72
Perfect score:   2802
Sequence:        1 MMMVRRGLLAWISRVVVLLV..........RHEIEAHLRKQKQKTSSKKT 532

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        251160 seqs, 211109531 residues

Total number of hits satisfying chosen parameters:       502320

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10063581/runat_06062006_121416_12300/app_query.fasta_1
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02h -USER=US10063581_@CGN_1_1_43_@runat_06062006_121416_12300
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Pending_Patents_NA_New:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pna/PCT_NEW_COMB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/pna/US06_NEW_COMB.seq:*
```

```
        3:  /EMC_Celerra_SIDS3/ptodata/2/pna/US07_NEW_COMB.seq:*
        4:  /EMC_Celerra_SIDS3/ptodata/2/pna/US08_NEW_COMB.seq:*
        5:  /EMC_Celerra_SIDS3/ptodata/2/pna/US09_NEW_COMB.seq:*
        6:  /EMC_Celerra_SIDS3/ptodata/2/pna/US10_NEW_COMB.seq:*
        7:  /EMC_Celerra_SIDS3/ptodata/2/pna/US11_NEW_COMB.seq:*
        8:  /EMC_Celerra_SIDS3/ptodata/2/pna/US60_NEW_COMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2740	97.8	3359	7	US-11-433-832-5826	Sequence 5826, Ap
2	370	13.2	282	7	US-11-433-832-46533	Sequence 46533, A
3	361.5	12.9	519	7	US-11-433-832-35532	Sequence 35532, A
4	220	7.9	182	7	US-11-433-832-25047	Sequence 25047, A
5	127	4.5	711	7	US-11-433-832-11536	Sequence 11536, A
6	109	3.9	3015	1	PCT-US03-41389-555	Sequence 555, App
7	109	3.9	3027	1	PCT-US03-41389-557	Sequence 557, App
8	107.5	3.8	6025	7	US-11-431-708-4455	Sequence 4455, Ap
9	107.5	3.8	6025	7	US-11-437-729-4648	Sequence 4648, Ap
10	107.5	3.8	6148	7	US-11-431-708-4449	Sequence 4449, Ap
11	107.5	3.8	6148	7	US-11-431-708-4452	Sequence 4452, Ap
12	107.5	3.8	6148	7	US-11-437-729-4636	Sequence 4636, Ap
13	107.5	3.8	6148	7	US-11-437-729-4650	Sequence 4650, Ap
14	107.5	3.8	6185	7	US-11-431-708-4451	Sequence 4451, Ap
15	107.5	3.8	6185	7	US-11-437-729-4982	Sequence 4982, Ap
16	107.5	3.8	6187	7	US-11-431-708-4443	Sequence 4443, Ap
17	107.5	3.8	6187	7	US-11-431-708-4454	Sequence 4454, Ap
18	107.5	3.8	6187	7	US-11-437-729-4631	Sequence 4631, Ap
19	107.5	3.8	6187	7	US-11-437-729-4647	Sequence 4647, Ap
20	107.5	3.8	6187	7	US-11-437-729-4649	Sequence 4649, Ap
21	107.5	3.8	6882	7	US-11-431-708-4448	Sequence 4448, Ap
22	107.5	3.8	6882	7	US-11-437-729-4635	Sequence 4635, Ap
23	107.5	3.8	6921	7	US-11-431-708-4453	Sequence 4453, Ap
24	107.5	3.8	6921	7	US-11-437-729-4658	Sequence 4658, Ap
25	107	3.8	5992	7	US-11-437-729-4632	Sequence 4632, Ap
26	105.5	3.8	2300	7	US-11-414-676-3	Sequence 3, Appli
27	105.5	3.8	2312	7	US-11-433-832-48093	Sequence 48093, A
28	105.5	3.8	3138	8	US-60-796-903-19	Sequence 19, Appl
29	105.5	3.8	4512	7	US-11-433-832-27189	Sequence 27189, A
30	105	3.7	5998	7	US-11-437-729-3901	Sequence 3901, Ap
31	105	3.7	7448	7	US-11-437-729-3902	Sequence 3902, Ap
32	105	3.7	7448	7	US-11-437-729-3903	Sequence 3903, Ap
33	105	3.7	8969	1	PCT-US03-41389-38	Sequence 38, Appl
34	104	3.7	2788	7	US-11-433-832-603	Sequence 603, App
35	103.5	3.7	14198	7	US-11-437-729-5075	Sequence 5075, Ap
36	102	3.6	1049	7	US-11-433-832-27654	Sequence 27654, A
37	101.5	3.6	1717	7	US-11-253-199-2166	Sequence 2166, Ap
38	101.5	3.6	3126	7	US-11-431-708-7018	Sequence 7018, Ap
39	101.5	3.6	13572	7	US-11-437-729-5073	Sequence 5073, Ap
40	101.5	3.6	13572	7	US-11-437-729-5077	Sequence 5077, Ap
41	101.5	3.6	13676	7	US-11-437-729-5076	Sequence 5076, Ap
42	101.5	3.6	13701	7	US-11-437-729-5074	Sequence 5074, Ap
43	101	3.6	2615	7	US-11-433-832-43944	Sequence 43944, A
44	100.5	3.6	2646	7	US-11-433-832-3897	Sequence 3897, Ap
45	100	3.6	6011	7	US-11-437-729-4638	Sequence 4638, Ap

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rnpm.

start

```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          June  6, 2006, 17:08:44 ; Search time 8394 Seconds
                                           (without alignments)
                                           5557.529 Million cell updates/sec

Title:           US-10-063-581-72
Perfect score:   2802
Sequence:        1 MMMVRRGLLAWISRVVVLLV..........RHEIEAHLRKQKQKTSSKKT 532

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        86534536 seqs, 29229259966 residues

Total number of hits satisfying chosen parameters:      173069072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10063581/runat_06062006_121413_12260/app_query.fasta_1
-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=rnpm -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02h -USER=US10063581_@CGN_1_1_7855_@runat_06062006_121413_12260
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Pending_Patents_NA_Main:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSA_COMB.seq:*
```

```
 2:  /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSB_COMB.seq:*
 3:  /EMC_Celerra_SIDS3/ptodata/2/pna/PCTUSC_COMB.seq:*
 4:  /EMC_Celerra_SIDS3/ptodata/2/pna/US075_COMB.seq:*
 5:  /EMC_Celerra_SIDS3/ptodata/2/pna/US076_COMB.seq:*
 6:  /EMC_Celerra_SIDS3/ptodata/2/pna/US077_COMB.seq:*
 7:  /EMC_Celerra_SIDS3/ptodata/2/pna/US078_COMB.seq:*
 8:  /EMC_Celerra_SIDS3/ptodata/2/pna/US079_COMB.seq:*
 9:  /EMC_Celerra_SIDS3/ptodata/2/pna/US080_COMB.seq:*
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14:  /EMC_Celerra_SIDS3/ptodata/2/pna/US085_COMB.seq:*
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28:  /EMC_Celerra_SIDS3/ptodata/2/pna/US096B_COMB.seq:*
29:  /EMC_Celerra_SIDS3/ptodata/2/pna/US096C_COMB.seq:*
30:  /EMC_Celerra_SIDS3/ptodata/2/pna/US097A_COMB.seq:*
31:  /EMC_Celerra_SIDS3/ptodata/2/pna/US097B_COMB.seq:*
32:  /EMC_Celerra_SIDS3/ptodata/2/pna/US098A_COMB.seq:*
33:  /EMC_Celerra_SIDS3/ptodata/2/pna/US098B_COMB.seq:*
34:  /EMC_Celerra_SIDS3/ptodata/2/pna/US099A_COMB.seq:*
35:  /EMC_Celerra_SIDS3/ptodata/2/pna/US099B_COMB.seq:*
36:  /EMC_Celerra_SIDS3/ptodata/2/pna/US099C_COMB.seq:*
37:  /EMC_Celerra_SIDS3/ptodata/2/pna/US099D_COMB.seq:*
38:  /EMC_Celerra_SIDS3/ptodata/2/pna/US099E_COMB.seq:*
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40:  /EMC_Celerra_SIDS3/ptodata/2/pna/US100B_COMB.seq:*
41:  /EMC_Celerra_SIDS3/ptodata/2/pna/US101_COMB.seq:*
42:  /EMC_Celerra_SIDS3/ptodata/2/pna/US102A_COMB.seq:*
43:  /EMC_Celerra_SIDS3/ptodata/2/pna/US102B_COMB.seq:*
44:  /EMC_Celerra_SIDS3/ptodata/2/pna/US103A_COMB.seq:*
45:  /EMC_Celerra_SIDS3/ptodata/2/pna/US103B_COMB.seq:*
46:  /EMC_Celerra_SIDS3/ptodata/2/pna/US103C_COMB.seq:*
47:  /EMC_Celerra_SIDS3/ptodata/2/pna/US103D_COMB.seq:*
48:  /EMC_Celerra_SIDS3/ptodata/2/pna/US103E_COMB.seq:*
49:  /EMC_Celerra_SIDS3/ptodata/2/pna/US103F_COMB.seq:*
50:  /EMC_Celerra_SIDS3/ptodata/2/pna/US104_COMB.seq:*
51:  /EMC_Celerra_SIDS3/ptodata/2/pna/US105_COMB.seq:*
52:  /EMC_Celerra_SIDS3/ptodata/2/pna/US106A_COMB.seq:*
53:  /EMC_Celerra_SIDS3/ptodata/2/pna/US106B_COMB.seq:*
54:  /EMC_Celerra_SIDS3/ptodata/2/pna/US107A_COMB.seq:*
55:  /EMC_Celerra_SIDS3/ptodata/2/pna/US107B_COMB.seq:*
56:  /EMC_Celerra_SIDS3/ptodata/2/pna/US107C_COMB.seq:*
57:  /EMC_Celerra_SIDS3/ptodata/2/pna/US107D_COMB.seq:*
58:  /EMC_Celerra_SIDS3/ptodata/2/pna/US107E_COMB.seq:*
59:  /EMC_Celerra_SIDS3/ptodata/2/pna/US107F_COMB.seq:*
60:  /EMC_Celerra_SIDS3/ptodata/2/pna/US107G_COMB.seq:*
61:  /EMC_Celerra_SIDS3/ptodata/2/pna/US108_COMB.seq:*
62:  /EMC_Celerra_SIDS3/ptodata/2/pna/US109A_COMB.seq:*
```

SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rnpbm.

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rnpbm.

start

Go Back to previous page

```
                        GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on:         June  6, 2006, 19:35:05 ; Search time 1804 Seconds
                                          (without alignments)
                                          5435.440 Million cell updates/sec

Title:          US-10-063-581-72
Perfect score:  2802
Sequence:       1 MMMVRRGLLAWISRVVVLLV..........RHEIEAHLRKQKQKTSSKKT 532

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10063581/runat_06062006_121420_12349/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US10063581_@CGN_1_1_1675_@runat_06062006_121420_12349 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Published_Applications_NA_Main:*
```

```
     1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
     2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
     3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
     4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
     5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
     6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
     7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
     8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
     9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
    10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
    11:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
    12:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
    13:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
    14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
    15:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
    16:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2802	100.0	1746	8	US-10-698-190-13	Sequence 13, Appl
2	2802	100.0	3877	3	US-09-989-722-380	Sequence 380, App
3	2802	100.0	3877	3	US-09-989-723-380	Sequence 380, App
4	2802	100.0	3877	3	US-09-989-279-380	Sequence 380, App
5	2802	100.0	3877	3	US-09-989-727-380	Sequence 380, App
6	2802	100.0	3877	3	US-09-989-731-380	Sequence 380, App
7	2802	100.0	3877	3	US-09-989-732-380	Sequence 380, App
8	2802	100.0	3877	3	US-09-991-073-380	Sequence 380, App
9	2802	100.0	3877	3	US-09-990-442-380	Sequence 380, App
10	2802	100.0	3877	3	US-09-991-163-380	Sequence 380, App
11	2802	100.0	3877	3	US-09-993-604-380	Sequence 380, App
12	2802	100.0	3877	3	US-09-990-456-380	Sequence 380, App
13	2802	100.0	3877	3	US-09-989-721-380	Sequence 380, App
14	2802	100.0	3877	3	US-09-992-598-380	Sequence 380, App
15	2802	100.0	3877	3	US-09-989-293A-380	Sequence 380, App
16	2802	100.0	3877	3	US-09-989-735-380	Sequence 380, App
17	2802	100.0	3877	3	US-09-990-444-380	Sequence 380, App
18	2802	100.0	3877	3	US-09-991-181-380	Sequence 380, App
19	2802	100.0	3877	3	US-09-989-730-380	Sequence 380, App
20	2802	100.0	3877	3	US-09-990-436-380	Sequence 380, App
21	2802	100.0	3877	3	US-09-993-687-380	Sequence 380, App
22	2802	100.0	3877	3	US-09-989-734-380	Sequence 380, App
23	2802	100.0	3877	3	US-09-997-653-380	Sequence 380, App
24	2802	100.0	3877	3	US-09-989-724-380	Sequence 380, App
25	2802	100.0	3877	3	US-09-989-728-380	Sequence 380, App
26	2802	100.0	3877	3	US-09-990-441-380	Sequence 380, App
27	2802	100.0	3877	3	US-09-993-667-380	Sequence 380, App
28	2802	100.0	3877	3	US-09-997-428-380	Sequence 380, App
29	2802	100.0	3877	3	US-09-997-666-380	Sequence 380, App
30	2802	100.0	3877	3	US-09-990-438-380	Sequence 380, App
31	2802	100.0	3877	3	US-09-990-562-380	Sequence 380, App
32	2802	100.0	3877	3	US-09-990-711-380	Sequence 380, App
33	2802	100.0	3877	3	US-09-989-726-380	Sequence 380, App
34	2802	100.0	3877	3	US-09-998-156-380	Sequence 380, App
35	2802	100.0	3877	3	US-09-990-437-380	Sequence 380, App

SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rnpbn.

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rnpbn.

start

```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          June  6, 2006, 19:36:54 ; Search time 31 Seconds
                                          (without alignments)
                                          3031.730 Million cell updates/sec

Title:           US-10-063-581-72
Perfect score:   2802
Sequence:        1 MMMVRRGLLAWISRVVVLLV..........RHEIEAHLRKQKQKTSSKKT 532

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters:       493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10063581/runat_06062006_121423_12406/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US10063581_@CGN_1_1_18_@runat_06062006_121423_12406 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Published_Applications_NA_New:*
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```
1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2802	100.0	3877	6	US-10-196-749-263	Sequence 263, App
2	2802	100.0	3877	7	US-11-101-316-71	Sequence 71, Appl
3	2798	99.9	3426	6	US-10-511-937-438	Sequence 438, App
4	529.5	18.9	4563	6	US-10-196-749-311	Sequence 311, App
5	253.5	9.0	1823	7	US-11-293-697-2080	Sequence 2080, Ap
6	108.5	3.9	1625	6	US-10-953-349-17058	Sequence 17058, A
7	106.5	3.8	1956	7	US-11-217-529-76687	Sequence 76687, A
8	106	3.8	5040	7	US-11-217-529-77055	Sequence 77055, A
9	106	3.8	10211	6	US-10-505-928-326	Sequence 326, App
10	105	3.7	1680	7	US-11-217-529-3752	Sequence 3752, Ap
11	105	3.7	2139	7	US-11-217-529-1868	Sequence 1868, Ap
12	105	3.7	5658	7	US-11-217-529-6026	Sequence 6026, Ap
13	101.5	3.6	1806	6	US-10-473-173-88	Sequence 88, Appl
14	101.5	3.6	5181	7	US-11-217-529-2050	Sequence 2050, Ap
15	100	3.6	1633	6	US-10-953-349-20987	Sequence 20987, A
16	99.5	3.6	1530	7	US-11-217-529-6054	Sequence 6054, Ap
17	99.5	3.6	1959	7	US-11-217-529-950	Sequence 950, App
18	98.5	3.5	1944	7	US-11-217-529-78837	Sequence 78837, A
19	97.5	3.5	2130	6	US-10-953-349-32290	Sequence 32290, A
20	96.5	3.4	1578	7	US-11-217-529-1912	Sequence 1912, Ap
21	95	3.4	798	7	US-11-217-529-77706	Sequence 77706, A
22	94.5	3.4	1964	6	US-10-196-749-177	Sequence 177, App
23	94.5	3.4	1964	7	US-11-101-316-41	Sequence 41, Appl
24	94	3.4	978	6	US-10-953-349-30985	Sequence 30985, A
25	94	3.4	2442	7	US-11-217-529-174312	Sequence 174312,
26	93.5	3.3	2481	7	US-11-217-529-82095	Sequence 82095, A
27	93.5	3.3	5028	7	US-11-217-529-5947	Sequence 5947, Ap
28	93	3.3	1416	7	US-11-217-529-80716	Sequence 80716, A
29	92.5	3.3	933	7	US-11-217-529-5139	Sequence 5139, Ap
30	92.5	3.3	2422	7	US-11-293-697-2067	Sequence 2067, Ap
31	92.5	3.3	12342	7	US-11-217-529-4644	Sequence 4644, Ap
32	92	3.3	2192	6	US-10-953-349-14231	Sequence 14231, A
33	92	3.3	3444	7	US-11-217-529-1079	Sequence 1079, Ap
34	91.5	3.3	2066	6	US-10-953-349-5914	Sequence 5914, Ap
35	91.5	3.3	2700	7	US-11-217-529-75493	Sequence 75493, A
36	91.5	3.3	3108	7	US-11-217-529-2842	Sequence 2842, Ap
37	91.5	3.3	4695	7	US-11-217-529-80934	Sequence 80934, A
c 38	91	3.2	1530	7	US-11-293-697-146	Sequence 146, App
39	91	3.2	1555	7	US-11-293-697-1871	Sequence 1871, Ap
40	91	3.2	1833	7	US-11-217-529-80544	Sequence 80544, A
41	91	3.2	3213	7	US-11-217-529-77018	Sequence 77018, A
42	91	3.2	3678	7	US-11-217-529-309	Sequence 309, App
43	91	3.2	7254	7	US-11-217-529-1173	Sequence 1173, Ap

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rni.

start

```
                         GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:          June  6, 2006, 17:07:30 ; Search time 293 Seconds
                                          (without alignments)
                                          5096.057 Million cell updates/sec

Title:           US-10-063-581-72
Perfect score:   2802
Sequence:        1 MMMVRRGLLAWISRVVVLLV..........RHEIEAHLRKQKQKTSSKKT 532

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10063581/runat_06062006_121410_12249/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02h -USER=US10063581_@CGN_1_1_204_@runat_06062006_121410_12249
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
```

```
 2:  /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2802	100.0	3877	3	US-09-991-181-380	Sequence 380, App
2	2802	100.0	3877	3	US-09-990-444-380	Sequence 380, App
3	2802	100.0	3877	3	US-09-997-333-380	Sequence 380, App
4	2802	100.0	3877	3	US-09-992-598-380	Sequence 380, App
5	2802	100.0	3877	4	US-09-989-735-380	Sequence 380, App
6	2802	100.0	3877	5	US-09-989-726-380	Sequence 380, App
7	2802	100.0	3877	5	US-09-997-514-380	Sequence 380, App
8	2802	100.0	3877	5	US-09-989-728-380	Sequence 380, App
9	2802	100.0	3877	5	US-09-997-349-380	Sequence 380, App
10	2802	100.0	3877	5	US-09-997-653-380	Sequence 380, App
11	2802	100.0	3877	5	US-09-989-293A-380	Sequence 380, App
12	1466.5	52.3	2352	4	US-10-094-749-254	Sequence 254, App
13	529.5	18.9	4563	3	US-10-012-231A-259	Sequence 259, App
14	529.5	18.9	4563	3	US-10-015-389A-259	Sequence 259, App
15	529.5	18.9	4563	3	US-10-006-768A-259	Sequence 259, App
16	529.5	18.9	4563	3	US-10-015-671A-259	Sequence 259, App
17	529.5	18.9	4563	3	US-10-015-393A-259	Sequence 259, App
18	529.5	18.9	4563	3	US-10-011-833A-259	Sequence 259, App
19	529.5	18.9	4563	3	US-10-006-041A-259	Sequence 259, App
20	529.5	18.9	4563	3	US-10-012-064A-259	Sequence 259, App
21	529.5	18.9	4563	4	US-10-015-392A-259	Sequence 259, App
22	529.5	18.9	4563	5	US-10-011-795B-259	Sequence 259, App
23	529.5	18.9	4563	5	US-10-015-386A-259	Sequence 259, App
24	529.5	18.9	4563	5	US-10-012-121A-259	Sequence 259, App
25	529.5	18.9	4563	5	US-10-006-485A-259	Sequence 259, App
26	529.5	18.9	4563	5	US-10-006-746A-259	Sequence 259, App
27	529.5	18.9	4563	5	US-10-012-752A-259	Sequence 259, App
28	529.5	18.9	4563	5	US-10-017-253A-259	Sequence 259, App
29	529.5	18.9	4563	5	US-10-015-519A-259	Sequence 259, App
30	529.5	18.9	4563	5	US-10-015-715A-259	Sequence 259, App
31	529.5	18.9	4563	5	US-10-007-236A-259	Sequence 259, App
32	215.5	7.7	2988	3	US-09-991-181-325	Sequence 325, App
33	215.5	7.7	2988	3	US-09-990-444-325	Sequence 325, App
34	215.5	7.7	2988	3	US-09-997-333-325	Sequence 325, App
35	215.5	7.7	2988	3	US-09-992-598-325	Sequence 325, App
36	215.5	7.7	2988	4	US-09-989-735-325	Sequence 325, App
37	215.5	7.7	2988	5	US-09-989-726-325	Sequence 325, App
38	215.5	7.7	2988	5	US-09-997-514-325	Sequence 325, App
39	215.5	7.7	2988	5	US-09-989-728-325	Sequence 325, App
40	215.5	7.7	2988	5	US-09-997-349-325	Sequence 325, App
41	215.5	7.7	2988	5	US-09-997-653-325	Sequence 325, App
42	215.5	7.7	2988	5	US-09-989-293A-325	Sequence 325, App

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rapn.

start

```
                         GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:         June  6, 2006, 18:27:46 ; Search time 25 Seconds
                                          (without alignments)
                                          681.506 Million cell updates/sec

Title:          US-10-063-581-72
Perfect score:  2802
Sequence:       1 MMMVRRGLLAWISRVVVLLV..........RHEIEAHLRKQKQKTSSKKT 532

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       131829 seqs, 32025636 residues

Total number of hits satisfying chosen parameters:      131829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Pending_Patents_AA_New:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/paa/PCT_NEW_COMB.pep:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/paa/US06_NEW_COMB.pep:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/paa/US07_NEW_COMB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/paa/US08_NEW_COMB.pep:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/paa/US09_NEW_COMB.pep:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/paa/US10_NEW_COMB.pep:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/paa/US11_NEW_COMB.pep:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/paa/US60_NEW_COMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                       %
Result          Query
```

No.	Score	Match	Length	DB	ID	Description
1	107.5	3.8	1652	7	US-11-437-729-2073	Sequence 2073, Ap
2	107.5	3.8	1938	7	US-11-431-708-635	Sequence 635, App
3	107.5	3.8	1938	7	US-11-431-708-645	Sequence 645, App
4	107.5	3.8	1938	7	US-11-431-708-646	Sequence 646, App
5	107.5	3.8	1938	7	US-11-437-729-2090	Sequence 2090, Ap
6	107.5	3.8	1938	7	US-11-437-729-2092	Sequence 2092, Ap
7	107.5	3.8	1938	7	US-11-437-729-2102	Sequence 2102, Ap
8	107.5	3.8	1954	7	US-11-431-708-647	Sequence 647, App
9	107.5	3.8	1954	7	US-11-437-729-2091	Sequence 2091, Ap
10	107.5	3.8	1972	7	US-11-431-708-640	Sequence 640, App
11	107.5	3.8	1972	7	US-11-431-708-641	Sequence 641, App
12	107.5	3.8	1972	7	US-11-431-708-644	Sequence 644, App
13	107.5	3.8	1972	7	US-11-437-729-2078	Sequence 2078, Ap
14	107.5	3.8	1972	7	US-11-437-729-2079	Sequence 2079, Ap
15	107.5	3.8	1972	7	US-11-437-729-2093	Sequence 2093, Ap
16	106	3.8	567	1	PCT-US03-41389-556	Sequence 556, App
17	106	3.8	582	1	PCT-US03-41389-558	Sequence 558, App
18	105.5	3.8	580	7	US-11-414-676-4	Sequence 4, Appli
19	105	3.7	1960	7	US-11-437-729-1248	Sequence 1248, Ap
20	105	3.7	1960	7	US-11-437-729-1249	Sequence 1249, Ap
21	105	3.7	1960	7	US-11-437-729-1250	Sequence 1250, Ap
22	105	3.7	2910	1	PCT-US03-41389-39	Sequence 39, Appl
23	103.5	3.7	4523	7	US-11-437-729-2574	Sequence 2574, Ap
24	103.5	3.7	4523	7	US-11-437-729-2576	Sequence 2576, Ap
25	101.5	3.6	2252	7	US-11-437-729-2577	Sequence 2577, Ap
26	101.5	3.6	2713	7	US-11-437-729-2573	Sequence 2573, Ap
27	101.5	3.6	2713	7	US-11-437-729-2578	Sequence 2578, Ap
28	101.5	3.6	2723	7	US-11-437-729-2575	Sequence 2575, Ap
29	100.5	3.6	848	7	US-11-437-212-41	Sequence 41, Appl
30	100.5	3.6	1296	1	PCT-US05-43307-1	Sequence 1, Appli
31	100.5	3.6	1296	7	US-11-437-212-43	Sequence 43, Appl
32	100.5	3.6	1296	7	US-11-284-930-1	Sequence 1, Appli
33	100.5	3.6	1300	1	PCT-US05-43307-15	Sequence 15, Appl
34	100.5	3.6	1300	1	PCT-US05-43307-16	Sequence 16, Appl
35	100.5	3.6	1300	1	PCT-US05-43307-17	Sequence 17, Appl
36	100.5	3.6	1300	1	PCT-US05-43307-18	Sequence 18, Appl
37	100.5	3.6	1300	1	PCT-US05-43307-19	Sequence 19, Appl
38	100.5	3.6	1300	7	US-11-284-930-15	Sequence 15, Appl
39	100.5	3.6	1300	7	US-11-284-930-16	Sequence 16, Appl
40	100.5	3.6	1300	7	US-11-284-930-17	Sequence 17, Appl
41	100.5	3.6	1300	7	US-11-284-930-18	Sequence 18, Appl
42	100.5	3.6	1300	7	US-11-284-930-19	Sequence 19, Appl
43	100.5	3.6	1301	1	PCT-US05-43307-20	Sequence 20, Appl
44	100.5	3.6	1301	1	PCT-US05-43307-21	Sequence 21, Appl
45	100.5	3.6	1301	1	PCT-US05-43307-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-11-437-729-2073
; Sequence 2073, Application US/11437729
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001606
; CURRENT APPLICATION NUMBER: US/11/437,729
; CURRENT FILING DATE: 2006-05-22

SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rapm.

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rapm.

start

```
                        GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:          June  6, 2006, 18:26:45 ; Search time 610 Seconds
                                           (without alignments)
                                           1331.706 Million cell updates/sec

Title:           US-10-063-581-72
Perfect score:   2802
Sequence:        1 MMMVRRGLLAWISRVVVLLV..........RHEIEAHLRKQKQKTSSKKT 532

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters:      8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_Main:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/paa/PCTUS_COMB.pep:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/paa/US066_COMB.pep:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/paa/US073_COMB.pep:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/paa/US074_COMB.pep:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/paa/US075_COMB.pep:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/paa/US076_COMB.pep:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/paa/US077_COMB.pep:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/paa/US078_COMB.pep:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/paa/US079_COMB.pep:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/paa/US080_COMB.pep:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/paa/US081_COMB.pep:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/paa/US082_COMB.pep:*
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                 14: /EMC_Celerra_SIDS3/ptodata/2/paa/US084_COMB.pep:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/paa/US085_COMB.pep:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*
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17:  /EMC_Celerra_SIDS3/ptodata/2/paa/US087_COMB.pep:*
18:  /EMC_Celerra_SIDS3/ptodata/2/paa/US088_COMB.pep:*
19:  /EMC_Celerra_SIDS3/ptodata/2/paa/US089_COMB.pep:*
20:  /EMC_Celerra_SIDS3/ptodata/2/paa/US090_COMB.pep:*
21:  /EMC_Celerra_SIDS3/ptodata/2/paa/US091_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rapbn.

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rapbn.

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                         GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.


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; Sequence 264, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey

SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rapbm.

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rapbm.

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                        GenCore version 5.1.9
             Copyright (c) 1993 - 2006  Biocceleration Ltd.


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Run on:         June  6, 2006, 18:38:06 ; Search time 187 Seconds
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; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rai.

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                        GenCore version 5.1.9
             Copyright (c) 1993 - 2006  Biocceleration Ltd.


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Run on:          June  6, 2006, 18:26:26 ; Search time 51 Seconds
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Post-processing: Minimum Match 0%
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.